GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd

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Search Notes
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No.
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Listing first 45 summaries
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10: gb pr: *

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  100.0 18
100.0 173165
100.0 190369
91.1 47636
91.1 92956
91.1 14233
91.1 165928
91.1 117278
91.1 303037
91.1 303037
91.1 303750
88.6 2217
85.6 2336
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AR534203

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AC014385

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AC023725

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AR534203 Sequence
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AC119908 Mus muscu
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AC119908 Drosophil
AL121811 Drosophil
AL023725 Drosophil
AC103725 Drosophil
AC105352 Drosophil
AC105352 Drosophil
AC105492 Drosophil
AC105492 Rattus no
AE016931 Bacteroid
AK063186 Oryza sat
AK063186 Oryza sat
CX053259 Sequence
AY052136 Drosophil
BT0101590 Drosophil
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ALIGNMENTS

RESULT 2 AR534203/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Matches Cy Db	JOURNAL P FEATURES SOURCE ORIGIN ONERY Match Best Local	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE	AR534202 LOCUS DEFINITION ACCESSION VERSION
AR534203 Sequence 2 from patent US 6733971. AR534203 AR534203.1 GI:53924251 Unknown. Unclassified. 1 (bases 1 to 18) 1 (bases 1 to 18) Beachy, P.A., Tsai, MJ., Tsai, S., Krishnan, V. and Chen, CH.	vative 0; Mismatc AATGCGCCG 18 AATGCGCCG 18	atent: US 6733971-A 1 11-MAY-2004; Location/Qualifiers 118 /organism="unknown" /mol_type="genomic DNA" 100.0%; Score 18; DB 6; Length 18; Similarity 100.0%; Pred. No. 12;	Unknown. Unknown. Unclassified. 1 (bases 1 to 18) 1 (bases 1 to 18) Beachy.P.A., Tsai,MJ., Tsai,S., Krishnan,V. and Chen,CH. Method for identifying an agent that affects a hedgehog signaling	AR534202 18 bp DNA linear PAT 08-OCT-2004 Sequence 1 from patent US 6733971. AR534202 AR534202.1 GI:53924250

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COMMENT
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AUTHORS
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AC125317/c
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                                                                                                                                                         Wilson,R.

Wilson,R.

Direct Submission

Submitted (13-NOV-2003) Department of Genetics, Washington
Submitted (13-NOV-2003) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Feb 23, 2003 this sequence version replaced gi:25167251.

Genome Center

Iniversity Genome Sequencing Center
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (23-FEB-2003) Genome Sequencing Center,
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 173185)
                                                                                                                                                                                                                                                                                                                                                                                                                                  McPherson, J.D. and Waterston, R.H.
Direct Submitsed (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park 4 (bases 1 to 173185)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                        Submitted (22-NOV-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 173195) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing of Mus musculus Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kruchowski,S., Meyer,R. and Doebber,A.
The sequence of Mus musculus BAC clone RP24-286L23
Unpublished (2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 173185)
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Mus musculus BAC clone RP24-286L23
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                                                                                                                          Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
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|mol_type="genomic_DNA"
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0; Mismatches
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu see

문 5

SOURCE INFORMATION:
The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert Location/Qualifiers

of the clone.

FEATURES

repeat_region source /rpt_family="B2" 11805. .11940 /rpt /rpt_family="B4" 8170. .8400 /rpt_family="B4" 6055. .6117 rpt_family="B4" 0342. .10527 /rpt_family="ERV1" 4465. .4750 rpt_fami rpt_family="ID" /rpt_family="B4" 4751. .5143 /rpt_family="L1" 4384. .4436 rpt_family="MaLR" 'rpt_family="MaLR" 901. .3478 rpt_tamily="L1" L413. .1655 /mol_type="genomic DNA /db_xref="taxon:10090" /chromosome="7" clone organism="Mus musculus" _family="L1" _family≃"MaLR' _family="L1" family="Alu" tamily="ID" family="Alu" _family="ERVL" _family="Alu one="RP24-286L23" one_lib="RPCI-24" _family="B4" ly="L2"

.family="B2"

.13038

repeat_region

repeat_region repeat_region repeat_region repeat_region repeat_region

family="B2" family="L1" family="B4"

14711

.14359

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family="MER1_type"
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RSS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barraen, S., Barrae, N., Bastlen, V., Bloom, T., Boguelavkiy, L., Boukhgelter, B., Brown, A., Camartel, J., Campopiano, A., Chang, J., Chargaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dakrellano, K., Devar, K., Diaz, J.S., Dodge, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gones, C., Kamat, A., Karatas, A., Kells, C., Lakoque, K., Lamarares, R., Kamat, A., Karatas, A., Kells, C., Lakoque, K., Lamarares, R., Kamat, A., Karatas, A., Kells, C., Lakoque, K., Lamara, L., Johnson, R., Jones, C., McCarthy, M., McSwan, P., McKerman, K., Meddrim, J., Mentue, L., Milova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norrus, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Ray, A., Santos, R., Schauer, S., Stolupback, R., Strauss, M., Sutramanian, A., Talamas, J., Tefsaye, S., Theodore, J., Topham, K., Tiavers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M.J., Young, G., Zainoun, J., Zenbek, L., Zimmer, A. and Zody, M., Direct Submitted (102-Myr.2002) Whitehead Institute/MIT Center for Genome Research, 320 charles Street, Cambridge, MA 02141, USA 102 charles Street, Cambridge, MA 02141, USA 102 charles, L., Edward, P., Corum, B., Dodge, S., Dode, P., Corum, B., Chang, J., Cooke, P., Corum, B., Candarata, J., Contag, J., Cooke, P., Corum, B., Chang, J., Gardam, J., Santae, J., Kells, C., Landers, T., Levine, R., Linda, C., Kanta, A., Karata, A., Kells, C., Landers, T., Levine, R., Linda, M., Lin
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 7, clone RP24-240G4
Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus chromosome 7, clone RP24-240G4, complete sequence.
AC119908
AC119908.16 GI:51921399
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18814

18983

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ICE 4 (bases I to 190369)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Barren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Barren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Barren, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Chang, T., Boguslavkly, L., Boukhgaiter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, P., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Grackson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Hagoslan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthaws, C., Murphy, T., Naylor, J., Maylor, J., Manning, J., Matthaws, C., Murphy, T., Naylor, J., Nguyen, T., Nicol, R., Norbu, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N. Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Zimmer, A., and Zody, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Submitted (nr. spen-2nna), whisher a standard cody, M., Schmer, A., and Zody, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Submitted (nr. spen-2nna), whisher a standard cody, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Submitted (nr. spen-2nna), whisher a standard cody, M., X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-SEP-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 8, 2004 this sequence version replaced gi:50839014. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Submitted (30-JUL-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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18; Conserv
1 GTTCTACATAATGCGCCG 18
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mplement(11516...
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28 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Adachi, J., Pikuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hyashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayiashida, K., Hayashida, Y., Iteda, R., Imamura, K., Katch, H., Kawagashira, N., Kawai, J., Kawamata, M., Kanagawa, S., Katch, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Mishi, S., Kunihara, C., Kurosaski, T., Kusumegi, T., Li, C., Lu, M., Mizuo, K., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Matsubara, K., Matsuyama, T., Mizhi, K., Nomura, K., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Noka, M., Ooka, H., Osaki, D., Sasaki, D., Satoh, K., Satoh, K., Shibata, K., Shinata, K., Sugina, A., Suzuki, K., Satoh, K., Satoh, K., Shibata, K., Sugina, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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                                                                                                                                                   Submitted (77-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchianias affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           japonica rice recess, and annotatio Science 301 (5631), 376-379 (2003) 22752273
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK109255 677 bp mRN.
Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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02-185-A05, full
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片 S

Query Match Best Local Similarity

Score 16.4; DB 2; Pred. No. 2.1e+02;

Length 47636;

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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                              Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10210737 by the submitter.
For further information on this sequence e-mail to fly@celera.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location(Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.
1 (bases 1 to 47636)
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AC014385.1 GI:6436950
HTG; HTGS PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster,
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Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCTACATCATGCGCCG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                      /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                        /mol_type="genomic_DN
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Oryza sativa/mol_type="mRNA"
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Pred. No. 1.5e+02;
0; Mismatches 1
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SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                     to fly@celera.com
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Matches

17; Conservative

0;

Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is a 'working draft' sequence. It currently consists of 178 contigs. The true order of the pieces is not known the contigs are represented as runs of N, but the exact sizes of sequence.

1 415 contig are represented as runs of N, but the exact sizes of sequence.

1 415 contig of 415 in length

516 515: gap of unknown length

1054 1308: contig of 438 in length

1054 1308: contig of 255 in length

1149 1448: contig of 40 in length

1249 1548: gap of unknown length

1259 2026: contig of 478 in length

2227 2126: gap of unknown length

2327 2326: contig of 520 in length

2327 2426: gap of unknown length

2328: contig of 532 in length

2329 2878: contig of 352 in length

2320 2878: contig of 352 in length

2321 288: gap of unknown length

2322 278: contig of 352 in length

2323: contig of 352 in length

2325: gap of unknown length

2326: contig of 352 in length

2327 278: contig of 352 in length

2328: gap of unknown length

2329 2878: gap of unknown length

2320 2878: gap of unknown length

2321 288: gap of unknown length

2322 278: contig of 352 in length

2323: contig of 352 in length

2325: gap of unknown length
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2027
2027
2127
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Sanger Centre, Wellcome Trust Genome Campus, Hinxton Hall, Hinxton, 2 (bases 1 to 92958)
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92958 bp DNA linear HTG 11-OCT-1999
Drosophila melanogaster chromosome X clone BACRIJJ17 map 4A strain
Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 178 unordered pieces.
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                                                    2878; gap of unknown length
3225; gap of unknown length
3257; contig of 32 in length
3257; contig of 32 in length
3257; contig of 38 in length
3257; contig of 38 in length
3250; gap of unknown length
4025; contig of 205 in length
4125; gap of unknown length
4575; contig of 450 in length
4575; contig of 497 in length
5572; gap of unknown length
5572; contig of 497 in length
5604; gap of unknown length
5604; gap of unknown length
6606; gap of unknown length
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6701; gap of unknown length
6901; contig of 355 in length
6901; contig of 300 in length
6901; contig of 400 in length
6901; contig of 400 in length
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10413: gap of unknown length
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16207: gap of unknown length
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16373: contig of 375 in length
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2: contig of 90 in length
2: contig of 90 in length
2: contig of 461 in length
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2: contig of 164 in length
2: gap of unknown length
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
gene
                                                                                                                                                                                        the identified CDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetrical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0406008 clone has an overlap with p0408003 (DDBJ: AP003241) at 5' end and with p0446B05 (DDBJ: AP003251) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp), URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Nov 20, 2001 this sequence version replaced gi.13027270.
Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTYNZ.0, BLASTYNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified TNA Scores with STASTP2.0. ESTs represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                         http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki, T., Matsumoto, T. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to 144233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Yamamoto, K.
                                                                                                                  (japonica cultivar-group)"
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Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
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The genome sequence and structure of rice chromosome 1

Nature 420 (6913), 312-316 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144233 bp DNA linear Oryza sativa (japonica cultivar-group) genomic DNA, PAC clone:P0406G08.
AP003240 BA000010
AP003240.2 GI:17026065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAFLAGESPPYSÄGDIEGMFIASMYKYARLISNULTYHLISHDEKCIKIOI ILKFIKORLATLIVIEVVOIQATANVSTCKVODEVSVVVEAAHPRDDILSVTEITEV (OMPLAMELT (Join (18872. 19012, 20426. 20452))
                                                                                                                                                                                                                   Join(21355. .21369,21742. .21913,23339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join (18872. .19012, 20426.
                                                                                                                                                                                   note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB86444.1"
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                                                                                                                                                                                                                                                      oin(21355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="P0406G08.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement (Join (9601 . .9724,10890 . .11155,11301 . .11727, 12366 . .1250,12604 . .12753,12831 . .12937,13045 . .13104, 13364 . .13543,13785 . .14009,14468 . .14596,14678 . .14755, 14829 . .14942,15084 . .15243,16237 . .16488,17615 . .17715), /gene="p0406608.3" /note="contains ESTs AU057528(S21533),AU057527(S21533)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGMEHGTWEMSESKHRVVLADKTYHGEIRVSLTFTASAKMYIQNIVES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVARDQGKNPSWNEVFKFQINSTAATGQHKLFLRLMDHDTFSRDDFLGEATINVTDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MAGSGYLEVHLVDAKGLTGNDFLGEIGKIDPYVVVQYRSQERKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative FIERG1 protein"

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PTTVLAMMSVPGAHQQRGRARDNPR"
join(6220...6298,6389. .6454,6573. .6711,7009. .7150,
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|gene="p0406G08.1"
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           165928 bp DNA linear INV 24-J
Drosophila melanogaster X BAC RP98-9110 (Roswell Park Cancer
Institute Drosophila BAC Library) complete sequence.
ACC02725
                                                                                                                                                                                                                                                                                                                                    l Similarity 94.4
17; Conservative
                                                                                                  AC023725
                                                                                                                                                                                                                                                                    GTTCTACATAATGCGCCG 18
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MALLAKLENLASNITRHFRLEGGDLDVTHDYGGKNPENCSCSSS SSRIKSPEKTPYDDGGRASFLSYLLYACDCETHIVTKPFPSLD" complement (join(36419. .36549,36655. .37629,38130. .38258,38416. .38660,38743. .38894,38995. .39096))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(34857. .35053,35343. .35412))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGAWPYDPTEFYQLQTKPVRENLPSQSSSFASSINGSSVTFSEGFESLLSPAGYLPDV
SLNDFVVQNQQALQFRRGFQEASKFLEDESKLVIDVDKLYSGDEGSRFLGSVAGSKKL
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LERMERÞETYKGMOVENORVGFKOLFLNODMMKRAREKVRCYHKDFIIDEDNRWLLOG
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HGVIHVPFOMRDACYHMPTWRKGPAAPLRRTTPSADVSLALFRASVRPACGSGVSGSG
PPRGAVGELGGQGNSVSVAFGEPGPCAV"
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                                                                                                                                                                                                                                                                                                                                             Score 16.4; DB 8; Length 144233; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                     RSS Worley, C.C., Adame, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooke, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blabrooke, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Che
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Muzny,D., Scherer,S., Adams,M.D., Holt,R.A., Evans,C.A.,

Gocayne,J.D., Tabor,P., Williamson,A., Homsi,F.H.,

Dugan-Rocha,S.D., Sodergren,E.S., Hodgson,A.H., Chen,R.C.,

Ayele,M., Scott,G.S., Worley,K.W., Amamatides,P.G., Brandon,R.C.,

Rogers,Y., An,H., Baldwin,D., Beeson,K.Y., Brown,M., Buhay,C.,

Rusam,D.A., Center,A., Chen,G., Chen,Z., Clerc-Blankenburg,K.,

Davenport,L.B., Dietz,S.M., Ding,Y., Dodson,K., Doup,L.E.,

Daveper,H., Emery-Cohen,A., Ferriera,S., Garg,N.D.S., Houck,J.,

Hostin,D., Howland,T.J., Hume,J., Ibegwam,C., Jalali,M., Kovar,C.,

Liu,W., Mattei,B., McIntosh,T.C., Morgan,M., Moy,M., Murphy,B.,

Nelson,K.A., Ndassa,Y., Nguyen,N., Perez,L., Pittman,G.S., Puri,V.,

Scheeler,F., Shen,H., Strong,R., Tector,C., Wang,Q., Williams,S.M.,

Wheeler,D., Weinstock,G., Gibbs,R. and Venter,J.C.
                          Submitted (17-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopeora; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                              Worley, K.C.
Direct Submission
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BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                           Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 24, 2002 this sequence version replaced gi:21306516. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-TAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 165928)
                                                                                                                                                    CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                         gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCM-HGSC
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Submitted (01-UUN-2002) Human Ger
of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
7 (bases 1 to 165928)
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s, Baylor College
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from
                      7:541-550) searches dbSTS, GDB, and
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of Medicine, One
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of a local database that local mapping efforts. Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse Bequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality strandards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: //www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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misc_feature
                                                                                       misc_feature
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101364. .101369
                                                                                           40955.
                                                                                                                           /organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|/mbl_type="genomic TONA"
|/db_xref="taxon:7227"
|chTomosome="X"
                                                                                                                                                                                                                    Location/Qualifiers
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                                                                          'note="Baylor,14T/Celera,15T'
                                                                                                          clone="RP98-9110"
                                                                                                                                                                                                     .165928
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Worley, K.C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burket, C., Burch, B., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chevez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elveland, C.D., Cox, C., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guaratre, P., Hale, S., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L., E., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Liu, W., Man, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Michell, T., Mohabbat, K., Mart, R., Martin, R., Martindale, A., Mugyen, N., Moser, M., Neal, D., Newtson, N., Oguhan, S., Rojubokan, J., Dickerson, E., Metson, N., Optiedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickerson, E., Mwokenkwo, S., Peery, J., Peters, L., Pickerson, E., Myokenkwo, S., Peters, L., Pickerson, R., Pickens, R., Putton, B., L., L., Chan, R., Payton, B., Peters, L., Pickens, R., Primus, E., Pu, L.L., Pickens, R., Pickens, R., Pojubokan, I., Rojfe, M., Pojes, M., Rojubokan, I., Rojfe, M., Poles, M., 
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Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Diny, Y., Dodson, K., Doup, L.E.,
Poters, S.M., Mong, Y., Dodson, K., Doup, L.E.,
Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalaii, M., Kovar, C.,
Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, O., Williams, S.M.,
Wheeler, J., Zaveri, J.S., Zhou, J., Zorrilla, S., Smith, H.O.,
Direct Shhmission
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1 (bases 1 to 172784)
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Prosophila melanogaster X BAC RP98-45017 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence.
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94.48;
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Pred. No. 2.3e+02;
0; Mismatches 1;
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TITLE JOURNAL REFERENCE AUTHORS NES 3 (bases 1 to 172784)

NES Worley, K. C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bornin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bornin, D., Bouck, J., Bouck, J., Brown, B., Byrant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Direct Submission
Submitted (01-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 172784) Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svattek,A., Tabor,P., Tanerisa,A., Tamerisa,K., Tangy,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas, S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warten,R., Washington,C., Wu,Y., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Wu,C., Wu,Y., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Vinson,R., Weinstock,G. and Gibbs,R.

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only

Submitted (12-JUN-2002) Human Genome Sequencing Center, Depa. of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jun 12, 2002 this sequence version replaced gi:18030112. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

Department

REFERENCE AUTHORS TITLE

JOURNAL

Submission

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

Direct Submission
Submitted (27-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 172784)
ECM-HGSC.

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KEYWORDS
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AC107403/c
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1 (bases 1 to 181831)

1 (bases 1 to 181831)

Muzny, D., Scherer, S., Adams, M.D., Holt, R.A., Evans, C.A.,

Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,

Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,

Ayele, M., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,

Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,

Busam, D.A., Center, A., Ding, Y., Dodson, K., Doup, L.E.,

Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,

Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J.,

Hostin, D., Howland, T.J., Hume, J., Ibogwam, C., Jalali, M., Kovar, C.,

Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Miscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC107403 181831 bp DNA linear INV 30-MA: Drosophila melanogaster X BAC RP98-21M21 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
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/chromosome="X"
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Pred. No. 2.3e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS Norley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Barbaria, J., Benrie, J., Billankenburg, K., Bonnin, D., Bouck, J., Bou
submitted (30-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 20, 2002 this sequence version replaced gi:20514404.
                                                                                                                                                                                                                                                Submitted (20-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                of Molecular and Human
Baylor Plaza, Houston,
5 (bases 1 to 181831)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Eukarycta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 309037)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D. Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.
                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                    complete sequence. AE003429 AE002566 AE003224 AE003327 AE014298 AE003429.3 GI:22831639
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Drosophila melanogaster chromosome
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17; Conserv
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCTACTTAATGCGCCG 134056
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Overlapping clones are noted at the beginning and end of the
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complement(102930, .181831)
/note="overlaps bases 87026,
/function="clone overlap"
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94.48;
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Pred. No. 2.3e+02;
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       Gocayne, J.D.,
.A., Galle, R.F.,
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                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 309037)
3 (bases 1 to 309037)
Misra,S., Crosby,M.A., Mungall,C.J., Matthews,B.B., Campbell,K.S., Misra,S., Crosby,M.A., Mungall,C.J., Millburn,G.H., Prochnik,S.E., Smith,C.D., Tupy,J.L., Whitfied,E.J., Bayraktaroglu,L., Berman,B.P., Bettencourt,B.R., Celniker,S.E., de Grey,A.D., Drysdale,R.A., Harris,N.L., Richter,J., Russo,S., Schroeder,A.J., Shu,S.Q., Stapleton,M., Yamada,C., Ashburner,M., Gelbart,W.M., Annotation of the Drosophila melanogaster euchromatic genome: a genome Biol. 3 (12), RESEARCH0083 (2002)
Genome Biol. 3 (12), RES 22426070
                                                                                                Kaminker, J.S., Bergman, C.M., Kronmiller, B., Svirskas, R., Patel, S., Frise, E., Wheeler, D.A. Rubin, G.M., Ashburner, M. and Celniker, S.E. The transposable elements of the Drosophila
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RESEARCH0084 (2002)
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AUTHORS

.7075,7150.

.6211,6429.

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REFERENCE
AUTHORS
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    repeat_region
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Gelbart, W.M.
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-SEP-2002) University of California Sciences Addition, Berkeley, CA 94720, USA
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Unpublished
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Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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AC128492.2 GI:23265132
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RATTUS NOTVEGICUS (NOTWAY rat)
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17; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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94.4%;
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Pred. No. 2.4e+02
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21-SEP-2002 PROGRESS

Benahmed, F.,

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Direct Submission

L Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Plaza, Houston, TX 77030, USA

On Sep 21, 2002 this sequence version replaced gi:21909220, and whole genome shotgun sequening reads assembled using Atlas (http://www.ligsc.bcm.tmc.edu/projects/rat/). As a result, the contigs that consist entirely of whole genome shotgun sequence contigs that consist entirely of whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dragard, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Eggar, A., Bacotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Gantar, R., Garcia, A., Garner, T., Gazza, M., Gebregorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Harvak, P., Hanes, A., Henderson, N., Hernandez, Y., Haland, W., Hamil, C., Hamilton, C., Hamilton, K., Wart, C., Liu, J., Jacob, L., Jiang, H., Johnson, B., Johnson, B., Howells, S., Hilyk, S., Hune, J., Idlebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Londson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Londson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Lorensuhewa, L., Lousseged, H., Lozado, R. J., Lu, X., Ma, J., Lw, Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Malloy, K., Martin, R., Martinez, E., Mallogave, S., McLeod, M. P., McKeill, T. Z., Meenen, E., Morris, S., Morris, S., Munidasa, M., Murphy, M., Nair, L., Narlis, S., Pasterrank, S., Polidexter, A., Popovic, D., Primus, B., Pull, L., Petez, A., Petez, L., Pfennhoch, C., Pulzo, M., Seery, A., Rose, M., Rose, R., Rizis, S., Parks, K., Polper, F., Polndexter, A., Popovic, D., Primus, B., Pull, L., Snedd, A., Sodergren, E., Song, X., Sotter, G., Shatsman, S., Shen, H., Shand, S., Vetz, V., Villasana, D., Walder, A., Tabor, P., Taylor, C., Sander, M., Surcis, S., Warren, J., Warren, R., Walder, B., Wang, J., Zhou, X., Zhou, X., Malcor, J., Warren, J., Walker, B., Wang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Von, V., Walse, R., Millson, R., Milcorn, K., Walder, B., Wang, J., Wang, J., Zhou, X., Sheh, J., Wang, J.,
                                                     Worley,K.C.

Direct Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 321355)
                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                ACCESSION
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Bacteroidaceae; Bacteroides.

1 (bases 1 to 303750)
Xu, J. Bjursell,M.K., Himrod,J., Deng,S., Carmichael,L.K.,
Chiang,H.C., Hooper,L.V. and Gordon,J.I.
A Genomic View of the Human-Bacteroides thetaiotaomicron Symbiosis
Science 299 (5615), 2074-2076 (2003)
                                                                                                                                                                Bacteroides thetaiotaomicron VPI-5482
Bacteroides thetaiotaomicron VPI-5482
Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales,
                                                                                                                                                                                                                                                                                                                              complete genome.
AE016931 AE015928
                                                                                                                                                                                                                                                                                                                                                                  AB016931 303750 bp DNA linear BCT 28-MAR-2003 Bacteroides thetaiotaomicron VPI-5482, section 6 of 21 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCTACATAATGCGCCG 18
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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317757. .319026
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complement(279655. .27
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clone_end:T7"
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clone_end:T7"
site:EcoRI
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lone_end:T7"
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                       GI:29338516
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94.4%; Pred. No. 2.4e+02;
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REFERENCE AUTHORS

JOURNAL

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COMMENT

TITLE JOURNAL REFERENCE

AUTHORS TITLE

(bases 1 to 321355)

JOURNAL

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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12663928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="minvrritylaflgagilpgisquesqueaqueque posityralqquemulpaqmdl gscipyalqque itrangremulpaqmdl gscipyalqque itrangreme posityralqque posityralqque itrangreme posityralqque posityralqque posityralqque posityralque posityralque posityralque posityralque posityrala propertionar properti
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GMEPNDOTVRNEMVDFWAAVATSPVAVNKFFHTVLSGWVLGGVFVVGISCWFLLKKRNR
EPALASIKIGAIFGLVSSLLAWTGDGSGYQIAQTQPWKLAAVGELYEGGTNVGLVGI
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PNVPLNFYAFRIMVILGGYFILFFIYULFFIYKKDLSKWRWHWHALLTIPLAYIAGO
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2132. .3523
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fpdflgdhftdadkgtyvgneliqralfekttdf"
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/locus_tag="BT1211"
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/locus_tag="BT1211"
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/protein_id="AAO76317.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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strain="VPI-5482"
                                                                                                                                                                                                                                                                                                                                                           locus_tag="BT1213"
575. .4804
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plement(87. .1649)
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ERSFIHHILAENETEVICEISNSNHPKNIMDKSGSGIGLEQVNRRLEILYPGQYTWQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNVSSSGQLIAGNNNYPSSVSGVGLEYLDIRQLSVESGDMFTEADIQSSAKVCVIGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MKKVIELQNIKRDFQVGBETVHALRGVSFTINEGEFVTIMGTSG
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VNNPAVILADEATGNLDTRTSFDILVLFQKLHAEGRTIIFVTHNPEIAQYSSRNIRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQATYDGAKAEFEYQKKNYERSKGLHDKSLISDTDYEQALYNYQKAKSAFDSSKASLA
KAERKLSYATITSPIDGVVISBDVEAGGTVASGGFETPIFFIAADLTQWQVVADVDEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6883. .7956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDLMTTLLACIAGISLVVGGIGIMNIMYVSVTERTREIGLRMSVGARGVDILSQFLIE
AIMISITGGLIGVIIGCGASWIVKSVAHWÞIFIQÞWSVFLSFAVCTVTGVFFGWYÞAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKRSIQQQISEMGSNMIMIHPGADRRGGVRQDPSAMQTLKLTDYEALRDETNFLSAIS
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4811. .5554
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                                                                                                                        EDDAKPILSLMSMKAMEELLPSSRFIRVHRSFIVQKDKIRVIDRGRIVFDKTYIPISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAADLDPIEAIRYE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ABC transporter, permease protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGHVIEDTVNTHVLSAAEALAALPKSDED"
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                                                                                                                                                                                                                                                                                                                                                                                locus_tag="BT1217"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              tag="BT1217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag="BT1215"
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codon_start=1

TITLE

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REFERENCE
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AK063186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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Best Local &
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, M., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Suzuki, S., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
                                                                                                                                                                                                                                                                                    AKO63186.1 GI:32973204
FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="METARSLIFHLVDIMNAEPDKTFNIAVSGGSTPALMFDLMANEY ADITPWKRMKLYWVDERCVPPEDSDSNYGMMRSLLLGIVPIPYENVFRIRGEVKPAKE AVRYSELVSQQVPKKNGWPEFDIVLLGAGDDGHTSSIFPGQEALLSSDQIYVTSTHPR NGQKRIAMTGEPILTARLVIFLITGKAKAEVVEEICHSGDTGPAAYIAHHAENVELFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENMFIGSPAGNTDRLLDFSTATTGTLFFVPSYDLLGELGE"
complement (11266. .11955)
/locus tag="BT1220"
complement (11266. .11955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNPFQNSFGGHIPQDVAGKQGENVIFIVYNLTDSPDTVDKVKDV
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VELSDEKKPGKAHNAYUTIGDDLKIVRANMPFATSKGEYGTYFIGYASTFSTTRRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="6-phosphogluconolactonase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (10131.
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TNSLTDYIDNTKHRMPAILTQEEEEKWLNPSLSKAEIASLLKPFDTEKMDAYVIRNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AA076326.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%; Score 16; DB 1;
100.0%; Pred. No. 4.2e+0
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 bp
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Thes 0; Indels
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A clone:001-112-B04, full
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                                                                                                       FEATURES
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COMMENT

source

/organism="Oryza sativa /mol_type="mRNA"

(japonica cultivar-group)"

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PUBMED
REFERENCE
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MEDLINE
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FALS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Marikawa, R., Niikura, J., Deda, M., Yu, R., Sugano, S., Yoshimura, A., Marikawa, R., Niikura, J., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Sugano, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hizamoto, K., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., KOjima, Y., Kondo, S., Konno, H., Kowa, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Incation/Onalifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 301 (5631), 376-379 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12869764
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Minimum
Maximum
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                                               N_Geneseq_16Dec04:*
1: geneseqn1980s:*
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18
1 GTTCTACATAATG
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(without alignments)
250.130 Million cell updates/sec
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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19	18	17	16	15	14	13	12	11	10	9	8	7	o	տ	4	ω	N	۳	Result No.
14.4	14.4	14.4	14.4	14.4	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	15.4	15.4	15.4	18	Score
80.0	80.0	80.0	80.0	80.0	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	85.6	85.6	85.6	100.0	Query
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ADS35791	ADS35874	ADS35721	ADS35825	ADS38863	ADS55711	ADS50197	ABD15782	ABD15757	ABD15682	ABD15713	ADR60599	AAA94133	AAA94156	AAX86622	ABA03041_01	ABL16076	ABL16077	AAX86621	ID
Ads35791 Human	_	Ads35721 Human aut	Ads35825 Human aut	Ads38863 Human aut	Ads55711 Bacteria	Ads50197 Bacterial	Abd15782 Pseudomor	Abd15757 Pseudomor	Abd15682 Pseudomon	Abd15713 Pseudomon	Adr60599 Cotton cD	Aaa94133 Adenoviru	Aaa94156 Adenoviru	Aax86622 Probe for	Continuation (2 o:	Abl16076 Drosophi	Abl16077 Drosophi	Aax86621 Sonic hed	Description

The present sequence represents a sonic hedgehog response element. The specification describes a transcription factor which is involved in a hedgehog-mediated signaling pathway, has at least one phosphorylation site and is dephosphorylated in response to the pathway. This

New transcription factors involved in hedgehog-mediated signaling, used to identify modulators for controlling expression of target genes, e.g.

WPI; 1999-494517/41.

Claim 3;

Page

49; 76pp;

English.

for treating cancer.

Beachy PA,

Tsai M,

Tsai SY,

Krishnan V,

Chen

45	44	43	42	41	40	c 39	38	37	c 36					c 31							24	23	22	c 21
14	14	14	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
77.8	77.8	&		80.03		•		80.01	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0
182	182	182	349980	349980	191284	110000	110000	110000	97662	67403	34827	8238	7967	7932	7914	7870	7846	6782	6782	5174	4076	1545	459	368
9	9	N	w	ω	12	11	ω	w	4	13	ω	13	13	4	13	13	13	13	4	σ	13	ω	w	N
ABL63025	ABL67930	AAT20207	AAF21612	AAF21611	ADQ97957	ACN43984_1	AAA81489_4	AAA81489_3	AAF83908	ADS36460	AAA81481	ADS34819	ADS34822	AAF83910	ADS34821	ADS34824	ADS34820	ADQ89799	AAF83909	AAS79419	ADS49496	ACA50831	AAZ54318	AAV20125
Abl63025 Breast ca	Abl67930 Ovary can	Aat20207 Human gen	Aaf21612 Neisseria	Aaf21611 Neisseria	Adq97957 Mouse can	Continuation (2 of	Continuation (5 of	Continuation (4 of	Aaf83908 Genomic s	Ads36460 Human aut	Aaa81481 N. mening	Ads34819 Human aut	Ads34822 Human aut	Aaf83910 cDNA sequ	Ads34821 Human aut	Ads34824 Human aut	Ads34820 Human aut	Adq89799 Antagonis	Aaf83909 cDNA sequ	Aas79419 DNA encod	Ads49496 Bacterial	Aca50831 Prokaryot	Aaz54318 Neisseria	Aav20125 Probe (26

ALIGNMENTS

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RESULT 1
AAX86621
ID AAX8
XX AAX8
XX AAX8
AC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sonic hedgehog response element; transcription factor; neuronal cell; hedgehog-mediated signaling pathway; proliferation; differentiation; proliferative disease; basal cell carcinoma; medulablastoma; meningioma; bone defect; polydactyly; jaw defect; rib defect; spina bifida; familial midline defect; cyclopia; neural tube defect; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sonic hedgehog response element nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX86621 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. (BAYU ) BAYLOR COLLEGE MEDICINE.
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RESULT 2
ABL16077/c
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     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL130511), expressed DNA ABBT6176-ABL30511), expressed DNA ABBT62727. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                             Claim 1; SEQ ID NO 42713; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                Venter JC, Adams м,
                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 42713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor binds to a hedgehog response element such as the present sequence. Modulation of the phosphorylation of the transcription factor is used to control expression of target genes involved in hedgehog differentiation of neuronal cells; treatment of proliferation or (specifically basal cell carcinoma, medullablastoma and meningioma); or bifida). Measuring the ratio of phosphorylated dephosphorylated forms of pathway-mediated familial middline defects (specifically cyclopia or pathway-mediated familial middline defects (specifically cyclopia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          2001-656860/75.
DB; ABB71974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology;
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                                                                                                                                                                                                                                                                                                PWD,
                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                               Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 2; Length 18, Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell signalling; insecticide;
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Sequence

1519

B₽;

306 A; 393 C;

410

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410 T;

0 U; 0 Other;

(Listeria monocytogenes EGD-e genome Accession Aba03041

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ABL16076/c

ID ABL16076/c

ID ABL16076;

XX ABL16076;

XX ABL16076;

XX ABL16076;

XX ABL16076;

XX Drosophila melanogaster expresse XX Drosophila melanogaster.

PN W0200171042-A2.

XX Drosophila melanogaster.

PN W0200171042-A2.

XX PP 23-MAR-2001; 2001WO-US009231.

XX PP 23-MAR-2001; 2000US-0191637P.

XX PF 23-MAR-2000; 2000US-0191637P.

XX
RESULT 4
ABA03041 01/c
ABA03041 101/c
Continuation (2 of 30) of ABA03041 from base 100001
WP Sequence split into 30 fragments LOCUS ABA03041
WP Fragment Name Begin End
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 4927 BP; 1288 A; 1106 C; 1081 G; 1452 T; 0 U; 0 Other:
                                                                                                                                                                                                                                                                                                                                                                                                                         useful in developmental biology and in elucidating cell signalling and insectively cell enteractions in higher eukaryotes for the development of discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA BB72072). The sequence data for this patent discretification of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 42710; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                               2 TTCTACATAATGCGCCG 18
                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                      Similarity
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16; Conservative
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94.1%;
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94.1%;
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Pred. No. 1.7e
0; Mismatches
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                         1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signalling; insecticide;
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Best 1
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                                                                                                                                                                                                                                                                                                                                   Sonic hedgehog response element; transcription factor; neuronal cell; hedgehog-mediated signaling pathway; proliferation; differentiation; proliferative disease; basal cell carcinoma; medullablastoma; meningioma; bone defect; polydactyly; Jaw defect; rib defect; spina bifida; familial midline defect; cyclopia; neural tube defect; probe; ss.
                                                                                                                                                                                                                              19-AUG-1999.
                                                                                                                                                                                                                                                                 WO9941281-A1
                                                                                                                                                                                                                                                                                                    Synthetic
                     WPI; 1999-494517/41
                                                        Beachy PA,
                                                                                           (UYJO
(BAYU
                                                                                                                                                  13-FEB-1998;
                                                                                                                                                                                       11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe for wild type sonic hedgehog response element.
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16; Conserv
                                                                                           UNIV JOHNS HOPKINS SCHOOL MEDICINE BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
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                                                      Tsai M,
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94.1%;
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Pred. No. 2.5e
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                                                        Krishnan V,
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o. 2.5e+02;
atches 1;
                                                        Chen
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New transcription factors involved in hedgehog-mediated signaling, used to identify modulators for controlling expression of target genes, e.g.
                                                                                                                       Example
                                                                                                                                    treating cancer.
                                                                                                                       8; Page 41; 76pp;
                                                                                                                       English
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transcription factor is used to control expression of target genes involved in hedgehog-mediated signaling pathway, specifically for regulating proliferation or differentiation of neuronal cells; treatment of proliferative diseases (specifically basal cell carcinoma, medullablastoma and meningioma); or to inhibit bone defects (e.g. polydactyly, jaw or rib defects, or spina bifida). Measuring the ratio of phosphorylated:dephosphorylated forms of transcription factor is used for diagnosis of hedgehog-mediated signaling pathway-mediated familial middles defects. The present sequence represents a probe for a wild type sonic hedgehog response element. The specification describes a transcription factor which is involved in a hedgehog-mediated signaling pathway, has at least one phosphorylation site and is dephosphorylated in response to the pathway. This transcription factor binds to a hedgehog response element such as sequence AAX86621. Modulation of the phosphorylation of the midline defects (specifically cyclopia or neural tube defects) least f of

Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

밁 Ś Query Match Best Local S Matches 16 16; Similarity **GTTCTACATAATGCGCCG** GTTCTACGTGATGCGCCG Conservative 82.2%; 0; 18 18 Score 14.8; Pred. No. 1 Mismatches .8e+02; 멂 <u>ب</u> Length Indels 18 0 Gaps 0

RESULT 6
AAA94156
AAA94166
AAA AAA94156 standard; DNA; 48 ₽₽

30-JAN-2001 (first entry)

Adenovirus 5 E1B promoter region vector PCR primer 世.

metastasis; liver tumour; Adenovirus 5 Ad 5; transcription factor Tcf binding site; r tumour; colorectal cancer; gene therapy; colon cancer; PCR primer;

Mastadenovirus.

WO200056909-A1

28-SEP-2000

24-MAR-2000; 2000WO-GB001142

24-MAR-1999; 99GB-00006815

(BTGI-) BIG INT LTD

Brunori 3

WPI; 2000-628270/60

transcription factor practices, factor binding sites, Viral DNA construct for treating neoplasms comprises tumor specific transcription factor binding sites in place of wild type transcription factor binding sites, operatively positioned in promoter region.

Page 30; 89pp; English

The present sequence is a PCR primer used during the construction of vector comprising the adenovirus 5 (Ad 5) E2 and E3 transcription sit This sequence was mutated so that the E1B promoter was replaced with copies of the Tcf transcription factor binding site. It is an example of a sites. 4

SSSSSSXXX

Sequence 48 BP; 9 A; 15 C; 7

Similarity

82.2%;

Score 14.8; Pred. No. 2.

2.1e+02;

DB 3; Length 48;

G; 17 T; 0 U; 0 Other;

the viral sequences of the invention, which are directed at tumour cells. They are able to replicate so that they do not need to be given in large quantities or inserted directly into the tumour, and those containing the Tcf binding site are particularly useful in treating colon cancer. In addition, metastases of the cancer, such as those found in the liver and colorectal cancers can be treated using gene therapy in a similar way

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Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
AAA94133
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Best Local S
Matches 16
                                                                                                                                                    The present sequence comprises the adenovirus EIB promoter. It has been mutated to form one of the preferred sequences of the invention, which are directed at tumour cells. These include sequences where the E2 promoter has been replaced with 4 copies of the Tcf transcription factor given in large quantities or inserted directly into the tumour, and those containing the Tcf binding site are particularly useful in treating colon liver and colorectal cancers can be treated using gene therapy in a
                                                                                                                              Sequence 180
                                                                                                                                                                                                                                                                                                                                            Viral DNA construct for treating neoplasms comprises tumor specific transcription factor binding sites in place of wild type transcription factor binding sites, operatively positioned in promoter region.
                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 21; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-628270/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000WO-GB001142.
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      111
                                                                  16;
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                                                                              Similarity
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GTCCTATATAATGCGCCG
                             GTTCTACATAATGCGCCG
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                                                             Conservative
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                                                                                                                           BP; 42
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                                                                                                                       A; 34 C;
                                                                          82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ElB promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 BP
                                                                                                                                                                                                                                                                                                                             English.
                          18
                                                           0;
                                                                       Score 14.8;
Pred. No. 2
                                                                                                                      40 G;
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                                                          Mismatches
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                                                                                                                      64 T;
                                                                    2.5e+02;
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(ZHOU/)
(CAOY/)
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12-DEC-2001; 2001US-00021323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cotton cDNA
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) ZHOU Y.
) CAO Y.
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; lignin;
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New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).

Claim 1; SEQ ID NO 1380; 14pp; English.

The invention relates to a recombinant polynucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification. CC Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property. Producing a plant having an improved property of the specification and producing a plant having an improved property of promoter region functional in a plant cell operably joined to a comprise region functional in a plant cell operably joined to a comprise region functional in a plant cell operably joined to a comprise region functional in a plant cell operably joined to a comprise region functional in a plant cell operably joined to a comprise region for a polypeptide associated useful for improving plant cold tolerance, manipulating growth rate in cold useful for improving plant cold tolerance, manipulating growth rate in compitation of plant proving plant disease, and the rate of homologous recombination or plant growth regulators), improving plant cold tolerance to plant disease, complant proving plant tolerance to proving plant tolerance to proving plant tolerance compitation of photosynthesis, modifying seed oil or protein yield complant growth and development under at least one stress condition. The constructs, in physical arrays of molecules, as plant breeding markers, in physical arrays of molecules, as plant breeding markers, in electronic format divacely from USPTO at collymucleotide sequence when intended specification, but was obtained collymucleotide sequence when intended specification, but was obtained collymucleotide sequence when a sequences were not prasent of this collymucleotides and all 58798 protein sequences were not prasent. le, the rem

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RESULT 9
ABD15713/c
ID ABD15713 standard; DNA; 1302 BP
XX
AC ABD15713;
AC Pseudomonas aeruginosa polynucl
XX
Bacterial infection; gene; ds;
AC ABD157195-B1.
AC ABD1
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                                                                                                                                                                                                                                                      The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therefore therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of pseudomonas species using biochip technology. Sequences ABD1197-CABD17967 represent P. aeruginosa polynucleotides of the invention. Note: specification but was obtained in electronic format from USPTO at
                                                                                       Query Match
Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                              Sequence 1302 BP; 238 A; 468 C; 386 G; 210 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 342 BP;
                                                                                                                                                                                                                                   seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 14317; 455pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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   GTTCTACATAATGCGCCG 18
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                                                                                    82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; ds; Pseudomonas aeruginosa infection;
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88.9%;
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                                                                                       Score 14.8; DB 11;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB 13;
Pred. No. 2.7e+02;
0; Mismatches 2;
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                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bush D;
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                                                                                                                Length 1302;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1479 BP; 288 A; 516 C; 444 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
27-JUL-1998;
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16; Conserv
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                              standard; DNA; 1566
                                                                                                                                                                             GCTCTATATAATGCGCCG
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                                                                                                                                                                                                                                                                                              Conservative
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                      82.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                            Score 14.8;
Pred. No. 3.
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RESULT 12
ABD15782
ID ABD15
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ABD15782
AC ABD15
XX
DT 29-JU
DT 29-JU
DX
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DE Pseud
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KW Bacte
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                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 16
        antibacterial
         Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                               Pseudomonas aeruginosa polynucleotide #14386.
                                                                                29-JUL-2004
                                                                                                                   ABD15782;
                                                                                                                                             ABD15782 standard; DNA; 1716 BP
                                                                                                                                                                                                                                                                                                                                                    Sequence 1566 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa polynucleotide #14361.
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                                                                                                                                                                                                                          GCTCTATATAATGCGCCG
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                                                                                (first
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                            283 A; 523 C; 513 G; 247 T; 0 U; 0 Other;
                                                                                entry)
                                                                                                                                                                                                                                                                                                   82.2%;
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Pred. No. 3.
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3.2e+02;
hes 2;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and CC therapy of pathological conditions, as molecular targets for diagnosis and CC prophylaxis and treatment of pathological conditions resulting from a CC bacterial infection, for evaluating a compound, such as a polypeptide, CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC including anti-P. aeruginosa drugs, as templates for recombinant CC production of P. aeruginosa drugs, as templates for routheast as target components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-CC ABD17967 represent P. aeruginosa polypucleotides of the invention. Note: The sequence data for this patent did not form part of the printed componence data for this patent did not format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
                                                                                                                                                                             Bacterial polynucleotide #4940.
                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                               ADS50197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1716 BP; 269 A; 499 C; 627 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 14386; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding Pseudomonas aeruginosa puseful as molecular targets for diagnostics, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathological conditions resulting from bacterial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                  GTTCTACATAATGCGCCG
                                                                                                                                                                                                                                                                            standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                             GCTCTATATAATGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THERAPEUTICS CORP
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98US-0094190P
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Pred. No. 3.3e+02;
0; Mismatches 2;
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d treatment of
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Bacteria

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RESULT 14
ADS55711/c
ID ADS55711;
XX ADS55711;
AC ADS55711;
XX DE Bacterial polynucleol
XX Recombinant DNA const
KW cold tolerance; heat
KW pathogen tolerance; i
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                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant DNA construct comprising a CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant thaving an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC thaving an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC plynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, pathogens or pests, increased resistance to plant disease, better growth rate by modification CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by conduction. This sequence represents a bacterial polymucleotide used in the scope of the invention. Note: The sequence data for this patent did cc not form part of the printed specification but was obtained in electronic format from USPTO at sequance.html.
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cao
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3057 BP; 652 A; 906 C; 949 G; 550 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 28627; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GOLD/)
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SLATER S
CHEN X.
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                                                                                                                                                                                                                                                                                            GTTCTACATAATGCGCCG 18
                                                                                                                                                                                                                                                              GTTGTACAGAATGCGCCG
                                                                     polynucleotide #7698
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                         CDNA; 3057
                                                                                                       entry
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                                                                                                                                                                                                                                                                                                                                            82.2%;
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                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 13;
Pred. No. 3.5e+02;
0; Mismatches 2;
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RESULT 15 ADS38863/c ID ADS388 XX AC ADS388 XX

ADS38863 standard; DNA; 201

ВP

ADS38863

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The invention relates to a recombinant DNA construct comprising a CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC transformed plant by the crombinant DNA construct and growing the transformed plant composition of producing a transformed plant composition of producing a transformed plant with the crombinant DNA construct and growing the transformed plant, where the CC improved plant properties, e.g. improved cold, heat or drought tolerance, cc increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved galactomannan cc condition, improved lignin production or improved galactomannan cc production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did cot form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                        Matches
                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                          Sequence 3057 BP; 652 A; 906 C; 949 G; 550 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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(SLAT/)
(CHEN/)
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                                                     GTTCTACATAATGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 31385; 122pp; English.
GTTGTACAGAATGCGCCG
                                                                                                                        Conservative
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2326
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Pred. No. 3
                                                                                                                        Mismatches
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                                                                                                                                                                              DB 13;
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16-DEC-2004

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Search completed: March Job time : 431 secs
                                                                                                                                                                                                                      CC The invention comprises amino acid and coding sequences containing CC genetic polymorphisms associated with an altered risk of developing an CC autoimmune disease (e.g. rheumatoid arthritis). The invention further CC comprises a method of identifying an individual that has an altered risk CR nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA CC treating autoimmune disease, such as: rheumatoid arthritis, type 1 CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory CR disease, psoriasis, thyroiditis, celiac disease, pernicious CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The CR present DNA sequence represents a human autoimmune disease-related CC genomic-based SNP context sequence of the invention. NOTE: The present CR sequence is not shown in the specification, but has been retrieved from xxx
                                                                                                                                  Query Match
Best Local S
Matches 15
                                                                                                                                                                                             Sequence 201 BP; 52 A; 37 C; 46 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; SEQ ID NO 4077; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cargill M, Begovich AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2003; 2003US-0455444P.
25-APR-2003; 2003US-0465241P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonaphritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APPL-) APPLERA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human autoimmune disease-related SNP context sequence - SEQ ID 4077.
                                                           125 TrcTACATAATGTGCC 110
                                                                                                                                    15;
                                                                                                  N
                                                                                                                                                   Similarity
                                                                                         TTCTACATAATGCGCC
                                                                                                                                 Conservative
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            'n
                                                                                                                      80.0%; Score 14.4; DB 13; Length 201;
93.8%; Pred. No. 4.3e+02;
tive 0; Mismatches 1; Indels 0
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Match Length
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Gapop 10.0 , Gapext 1.0
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18
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                     92387
151295
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818128
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US-09-916-91A-14317
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US-09-252-991A-14366
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US-09-949-016-14559
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Sequence 2, Appli
Sequence 1, Appli
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Sequence 3, Appli
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US-09-023-249-1
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US-09-583-110-1890	US-09-107-532A-551	US-09-252-991A-12375	US-09-513-999C-33885	US-09-949-016-14567	US-09-949-016-14566	US-09-949-016-14565	US-09-949-016-14564	US-09-949-016-14562	US-09-949-016-14561	US-09-949-016-14560	US-09-949-016-14559	US-09-949-016-14558	US-09-949-016-14557	US-09-949-016-14556	US-09-949-016-14555	US-09-949-016-14554	US-09-949-016-14553
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
1890, Ap	551, App	12375, A	33885, A	14567, A	14566, A	14565, A	14564, A	•	14561, A	14560, A	•	-	14557, A	14556, A	•	14554, A	14553, A

ALIGNMENTS

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Sequence 1, Application US/09023249A
Patent N. 627566
Pat
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Sequence 1, Application US/09934035
                                                                                                                    Query Match
Best Local Similarity 100.00
Watches 18; Conservative
                        RESULT 3
US-09-934-035-1
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                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-98
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: JHU1510-
TELEPHONE: 858/677-1456
INFORMATION FELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 2:
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US-09-023-249-2/c
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Patent No. 6277566
GENERAL INFORMATION:
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY NUMBER OF SEQUENCES: 8
                                                                                      18
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                                                                                                    1 GTTCTACATAATGCGCCG 18
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                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 BASE PAIRS
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FILING DATE: 13-Feb-1998
CLASSIFICATION: Application
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COUNTRY: U.S.A.
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STATE: CA
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Tsai, Sophia Y.,
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Krishnan, Venkatesh,
Chen, Chien-Huan
                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                   100.0%; Score 18; DB 3; Length 18; 100.0%; Pred. No. 0.5;
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RESULT 4
US-09-934-035-2/c
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Patent No. 6733971
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6733971
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION DATA:
APPLICATION NUMBER: US/09/934,035
FILING DATE: 21-Aug-2001
CLASSIFICATION BATA:
APPLICATION NUMBER: 09/023,24949
FILING DATE: 1998-02-13
APPLICATION NUMBER: 09/023,24949
FILING DATE: 1998-02-13
APPLICATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: JHU1510-1
TELLEPAX: 858/677-1456
TELLEPAX: 858/677-1465
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego
                                                                                                                                     APPLICANT: Beachy, Philip A.,
APPLICANT: Beachy, Philip A.,
Tsai, Sophia Y.,
Tsai, Ming-Jer,
Krishnan, Venkatesh,
                                                                                    Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Beachy, philip A.,
Tsai, Sophia Y.,
Tsai, Ming-Jer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                              1 GTTCTACATAATGCGCCG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 18; DB 4; Length 18; 100.0%; Pred. No. 0.5; tive 0; Mismatches 0; Indels
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                                                                                            PATHWAY
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ZIP: 92121
COMPUTER READABLE FORM:
WENTIM TYPE: Floppy disk

COUNTRY:

U.S.A.

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RESULT 5
US-09-023-249-3
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: both
    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,249A
FILING DATE: 13-Feb-1998
CLASSIFICATION: Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haile, Lisa A.
RECISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: JHU1510-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEPAX: 858/677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/934,035
PILING DATE: 21-Aug-2001
CLASSIPICATION: Application
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                              AL INFORMATION:
APPLICANT: Beachy, Philip A.,
TEAL. Sophia Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/023,24949 FILING DATE: 1998-02-13 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: genomic DNA
PRIOR
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 GTTCTACATAATGCGCCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                      STATE: CA
                                                                                                                                                                                                                                                       CITY: San Diego
                                                                                                                                                                                                                COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Krishnan, Venkatesh,
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Pred. No. 0.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Applicatio Patent No. 6733971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                    PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 09/023,24949

FILING DATE: 1998-02-13

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Liea A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: JHU1510-1
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: PATCHIEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-98
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: JHU1510-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beachy, Philip A.,
Tsai, Sophia Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTTCTACATAATGCGCCG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/934,035
FILING DATE: 21-Aug-2001
CLASSIFICATION: Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09934035
                                                                       ENGTH: 18 BASE PAIRS
                                                                                                                              TELEFAX: 858/677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDDRESSEE: Gray Cary Ware & Freidenrich LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Chien-Huan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsai, Ming-Jer,
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88.9%;
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Pred. No. 38;
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                                                                                                      ; TYPE: DNA
; ORGANISM: Adenovirus VR5
US-09-916-510A-7
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-30
                                                       Matches
                                                                  Query Match
Best Local
                                                                                                                                            SEQ ID NO 7
LENGTH: 180
                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09916510A Patent No. 6544507 GENERAL INFORMATION:
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                                                                                                                                                                        FILE REFERENCE: 604-596
CURRENT APPLICATION NUMBER: US/09/916,510A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: GB 9906815.7
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 9006815.7
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                    APPLICANT: IGGO, RICHARD D.
APPLICANT: BRUNORI, MICHELE A.
TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                    SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 1GGO, RICHARD D.
APPLICANT: BRUNORI, MICHELE A.
TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
FILE REFERENCE: 604-596
CURRENT FILING DATE: 2001-07-30
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 65445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 48
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  111
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                                                               Similarity
                      GTTCTACATAATGCGCCG 18
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                                                   Conservative
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128
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                                                              Score 14.8;
Pred. No. 5
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Pred. No. 46
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Pred. No. 38;
                                                 Mismatches
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                                                                      Length 180;
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US-09-252-991A-14361
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14317
SEQ ID NO 14317
LENGTH: 1302
                       Sequence 14361, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14317
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US-09-252-991A-14317/c
; Sequence 14317, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 14286
                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                      Query Match
CURRENT APPLICATION NUMBER: US/09/252,991A
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                            158 GCTCTATATAATGCGCCG 141
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                                                                                                                                                                                                                                                                                   1 GTTCTACATAATGCGCCG 18
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Pred. No. 85;
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Pred. No. 83
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14361
LENGTH: 1566
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
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US-09-252-991A-14361
                               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR TILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR TILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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LENGTH: 1716
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Best Local (
SEQ ID NO
                                                                                                                                                                                                                                                                                                                   Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                  SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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88.9%;
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88.9%;
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Pred. No. 8
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Pred. No. 86;
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(9287)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-14563
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US-09-949-016-14568
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                                                                                                                                                                                                                                                                                                                                            US-09-949-016-14569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                             Sequence 14569, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14568,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(151295)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JENGTH: 151295
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15; Conserv
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Pred. No. 3.3e+02;
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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14569

LENGTH: 151295

TYPE: DNA

CORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(151295)

COTHER INFORMATION: n = A,T,C or G

US-09-949-016-14569

Query Match
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

TTCTACATAATGCGCC 17

Db

73070 TTTTACATAATGCGCC 73085

Search completed: March 2, 2005, 04:45:46

Job time: 137 secs
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 Bummaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
           US-10-677-982-1
18
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/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USOC_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USOC_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USOC_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15.4 15.4	15.4 15.4	16.4	18 18	18	Score
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18	18 17	18	17	9 9	DB
US-10-437-963-10575 US-10-767-701-9687	US-10-425-115-128320 US-10-424-599-4803	US-10-425-115-164709 US-10-425-115-42326	US-10-677-982-1 US-10-677-982-2 US-10-437-963-13834	US-09-934-035-1 US-09-934-035-2	ID
Sequence 10575, A Sequence 9687, Ap		Sequence 164709, Sequence 42326, A		Sequence 1, Appli Sequence 2, Appli	Description

ALIGNMENTS

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RESULT 2
US-09-934-035-2/c
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Patent No. US20020102646A1
GENERAL INFORMATION:
APPLICANT: Beachy, Philip A.,
                                                                                                                                                                                        TELEPHONE: 858/677-145
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/934,035
FILING DATE: 21-Aug-2001
CLASSIFICATION PAPPLICATION PAPPLICATION PAPPLICATION PAPPLICATION DATA:

PRIOR APPLICATION NUMBER: 09/023,24949
FILING DATE: 1998-02-13
ATTORNEY/AGENT INFORMATION:
NAME: Haile Fiee P
                                                                                                                                                                                                                                                                             ALLOWAND AND THE PROPERTY OF T
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TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                            STRANDEDNESS: both
                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTTCTACATAATGCGCCG 18
                                                                                                                                                        LENGTH: 18 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsai, Sopnia ..
Tsai, Ming-Jer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krishnan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                         JHU1510-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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US-10-677-982-1
                    Matches
                                                      Query Match
                                                                                                                                                                                                   TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-677-982-1
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                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: JEM PC compatible
OPERATING SYSTEM: Windows95
CURRENT APPLICATION SATA:
APPLICATION LOATA:
APPLICATION NUMBER: US/10/677,982
FILING DATE: 01-Oct-2003
CLASSIFICATION NUMBER: US/09/023,249A
APPLICATION NUMBER: US/09/023,249A
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 09/023,249A
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 09/023,249A
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-198
APPLICATION NUMBER: 38,349
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: JHU1510-1
TELEPHONE: 858/677-1456
TELEPHONE: 858/677-1456
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                                                                                            LOCATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                          MOLECULE TYPE: genomic DNA FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsai, Sophia Y.,
Tsai, Ming-Jer,
Krishnan, Venkatesh,
Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                 Similarity
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                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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                Conservative
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                              100.0%;
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     Score 18; DB 1
Pred. No. 5.5;
0; Mismatches
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                                     _DB 17; Length 18;
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GTTCTACATAATGCGCCG 18

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US-10-677-982-2/c
                                                                        Sequence 12834, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/023,249A
FILING DATE: 13-Feb-1998
APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-98
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: HU1510-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA FEATURE:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                               n 100.0%;
Similarity 100.0%;
18; Conservative 0
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                                                                                                                                                                                                                                             GTTCTACATAATGCGCCG 18
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FILING DATE: 01-Oct-2003
CLASSIFICATION: Application
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TELEPAX: 858/677-1465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 BASE PAIRS
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Pred. No. 5.5;
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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 164709

LENGTH: 767
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Sequence 42326, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Local Similarity 94.4%;
Nes 17; Conservativa
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                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
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94.4%;
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Pred. No. 69;
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Pred. No. 60
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104341C.1
US-10-424-599-4803
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                                APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
FUNDBER OF SEQ ID NOMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 4803
LENGTH: 533
TYPE: DNA
ORGANISM: Glycine max
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US-10-425-115-128320
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APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yoinua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 128320
LENGTH: 379
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; OTHER INFORMATION: Clone ID: MRT4577_138602C.1
US-10-425-115-42326
                                                                                                                                                                                                                                                                                                                                                  Sequence 4803, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local
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SEQ ID NO 42326
LENGTH: 879
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ORGANISM: Zea mays
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Local Similarity 94.4%;
es 17; Conservative
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94.1%;
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Pred. No. 2.3e+02;
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Pred. No. 7
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RESULT 11
US-10-767-701-9687
; Sequence 9687, Application US/10767701
; Publication No. US20040172684A1
                                                                             ; OTHER INFORMATION: Clone ID: US-10-767-701-9687
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          Best Loc
Matches
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                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9687
LENGTH: 957
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Vinna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10575, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local
                                                                                                               ORGANISM: Sorghum bicolor FEATURE:
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ORGANISM: Oryza sativa
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                         Local
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                          Similarity
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Cao, Yongwei
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Barbazuk, Brad
        Conservative
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llarity 94.1%;
Conservative
85.6%; Score 15.4; DB 18; Length 957; 94.1%; Pred. No. 2.6e+02; tive 0; Mismatches 1; Indels 0
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94.1%;
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Pred. No. 2.6e+02;
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Pred. No. 2.4e+02;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 918;
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TTCTACATAATGCGCCG 18

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357 TTCTACATCATGCGCCG 373

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RESULT 13
US-09-934-035-3
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
PILE REFERENCE: 38-21(53322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 86671
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Patent No. US20020102646A1
GENERAL INFORMATION:
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Best Local (
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TYPE: DNA
ORGANISM: Zea mays
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                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/934,035
FILING DATE: 21-Aug-2001
CLASSIFICATION APPLICATION DATA:
PRIOR APPLICATION OBTA:
APPLICATION NUMBER: 09/023,24949
FILING DATE: 1998-02-13
APPLICATION NUMBER: 09/023,24949
FILING DATE: 1998-02-13
AFTORMEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
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ADDRESSEE: Gray Cary Ware & Freidenrich LLP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beachy, Philip A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4365 Executive Drive, Suite 1600
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Tsai, Ming-Jer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krishnan, venkar
Chen, Chien-Huan
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94.1%;
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Pred. No. 2.6e+02;
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RESULT 14
US-10-677-982-3
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Matches 16; Conserv
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Publication No. US20040082036A1
      Matches
                                          Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/677,982
FILING DATE: 01-Oct-2003
CLASSIFICATION: Application
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/023,249A
FILING DATE: 13-Feb-99
APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-99
APPLICATION NUMBER: 09/023,249
FILING DATE: 13-Feb-99
APPLICATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
y Match 82.2%;
Local Similarity 88.9%;
hes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, Chien-Huan
TITLE OF INVENTION: MODULATION OF HEDGEHOG-MEDIATED SIGNALING PATHWAY
NUMBER OF SEQUENCES: 8
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                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 18 BASE PAIRS
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MEDIUM TYPE: Floppy disk
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Tsai, Sophia Y.,
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 858/677-1456
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                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
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    Score 14.8; D
Pred. No. 3.4e
0; Mismatches
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Pred. No. 3.4e+02
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                      3.4e+02;
                                        DB 17; Length 18;
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Qy | GTYCTACATAATGCGCCG 18

RESULT 15
US-09-916-510A-30
RESULT 15
US-09-916-510A-30
RESULT 15
REPALT NO. US20020168349A1
REPAIR NO. UNMBER: US209/916,510A
CURRENT APPLICATION NUMBER: US209/916,510A
CURRENT APPLICATION NUMBER: US209/916,510A
CURRENT APPLICATION NUMBER: US209/916,510A
RODE RILING DATE: 1999-03-24
REPAIR NO. US2010 NO. US2010
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Minimum
Maximum
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219.461 Million cell updates/sec
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(c) 1993 - 2005
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85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	85.6	88.9	91.1	91.1	91.1	91.1	91.1		91.1	91.1
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ALIGNMENTS

REFERENCE AUTHORS RESULT 1 CO223769/c LOCUS FEATURES SOURCE ORGANISM COMMENT KEYWORDS ACCESSION DEFINITION VERSION JOURNAL source Picea sitchensis (Sitka spruce)

Elica sitchensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1. (bases 1 to 497)

E. 1. (bases 1 to 497)

E. Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R.,

Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R.,

Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M.,

Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E.,

Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C.,

Ritland, K. and Bohlmann, J.

The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries Genome BC forest genomics program University of British Columbia UBC Biotechnology Laboratory, 6174 University Boulevard, Vancouver, British Columbia, Canada, V6T 1Z3 Tel: 1-604-822-0282 Fax: 1-604-822-6097 WS01019.B21_O15 SS-R-N-A-11 Picea sitchensis cDNA clone WS01019_O15 POLYA=Yes Email: bohlmann@interchange.ubc.ca Plate: WS01019 row: O column: 15 Unpublished (2004)
Contact: Joerg Bohlmann CO223769.1 GI:49046084 quality sequence stop: /db_xref="taxon:332"
/clone="WS01019_015"
/sex="Hermaphrodite"
/sex="Hermaphrodite"
/tissue_type="Young root growth (terminal 1-3 cm) and old root growth (distal to terminal 1-3 cm) tissues"
/dev_stage="three year old clonal trees grown under greenhouse conditions in standard potting soil mixture."
/lab_host="E. coli DH10B cells" /organism="Picea sitchensis" /mol_type="mRNA" /cultivar="Gb2-229" Location/Qualifiers sequence tags from Tracheophyta; Picea. Rm. 237,

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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmprattuga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of RNA prepared and library constructed by W. Walter Lorenz, School of Porestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polya.

Seq primer: JENREV (CAGGAACAGCTATGACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An EST database from well-watered loblolly pine (Pinus taeda)
Unpublished (2003)
Other_ESTS: RTWM1 12 A07.b1 A015
Contact: Cordonnier-Pratt M
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neale, D.
An EST d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus; 1 (bases 1 to 522)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF401440 522 bp mRNA linear EST 29-AUG-2003 RTWW1_12_A07.g1 A015 Well-watered loblolly pine roots WW1 Pinus taeda cDNA clone RTWW1_12_A07_A015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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Pinus taeda
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/db xref="taxon:3352"
/db xref="taxon:3352"
/clone="RTWW1_12_A07_A015"
/lab_host="PHIOB-T1 phage-resistant E. coli"
/lab_host="PHIOB-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots WW1"
/note="Vector: pSI1180, Site 1: EcoRI; Site 2: XhoI; The
/ibrary was prepared from poTyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
                                                                                                                                                                                                                                                                        strain="CCLONES"
                                                                                                                                                                                                                                                                                                                               organism="Pinus taeda"/
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                        _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No.
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COMMENT

REFERENCE

AUTHORS

RESULT 2 CF401440

ACCESSION

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ORIGIN

FEATURES

Best Loca Matches

Query Match Best Local Similarity

100.0%; Score 18; DB ilarity 100.0%; Pred. No. 24; Conservative 0; Mismatchi-

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5159424 Clone ID:
GQ0014b B01 Clones available through: John MacKay, Ph. D.
Professeur adjoint -Assistant professor EMAIL:
jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
(Forest Biology Research Center) Universite Laval Quebec, Quebec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 4b row: 01 column: B
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 530)

Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and MacKay, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANADA G1K 7P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4 Fax: 418 656 7493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centre de Recherche en Biologie Forestiere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQ0014b.BR_B01 GQ001: Male strobili developmenta glauca cDNĀ clone GQ0014b_B01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: John MacKay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTTCTACATAATGCGCCG 18
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Picea glauca
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/tissue_type="Entire strobilus"
/dev stage="Three stages of preformed male strobili at end of winter dormancy were pooled: swollen fully closed buds, partly open buds and fully open buds"
/lab host="E. coli DH10B cells"
/clone lib="GQ001: Male strobili developmental sequence"
/note="Gy001: Male strobili, Vector: pBluescript
II SK (+) XR; Site_1: Eco-RI; Site_2: Xho-I; cDNA was
prepared from 5 mg of poly A+ selected RNA and was
directionally ligated into the pBluescript II SK (+) XR
vector (Stratagene), transformed by electroporation into
DH10B cells (In vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                organism="Picea glauca"
/mol_type="mRNA"
/strain="Tree 13-271"
/db xref="taxon:3330"
/clone="GQ0014b B01"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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i developmental
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                                                     DEFINITION
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                                                                                                                                                                                                        149
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GQ0014b.TB B01 GQ001: Male strobili developmental glauca cDNA clone GQ0014b_B01 3', mRNA sequence. CK443141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of FORESTY, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Unpublished (2003)
Other_ESTs: RTWW1_12_A07.g1_A015
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Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Pratt, L., Cordonnier-Pratt, M.-M., Mhite, T., Davis, J. and Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13-21 (TGTAAAACGACGGCCAGT)
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pinus taeda (loblolly pine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neale,D.
An EST database from well-watered loblolly pine (Pinus taeda) roots
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                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3352"
/clone="RTPWI 12 A07 A015"
/lab host="DHIGB-T1 phage-resistant E. coli"
/lab host="DHIGB-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots WW1"
/note="Vector: pSL1180; Site 1: EcoRI, Site 2: KhoI; The
library was prepared from poTyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL1180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."
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/mol tyme="mpNA"
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/strain="CCLONES"
                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 7; Length 573; 100.0%; Pred. No. 24;
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Pinus; Pinus.
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Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and MacKay, J.

Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Picea glauca (white spruce)
picea glauca
picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
1 (bases 1 to 638)
Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kir
Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jmackay@revs.ulaval.ca (Center for Computational Genomics and Bioinformatics (CCGB), Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN5159425 Clone ID: GQ00014b B01 Clones available through: John MacKay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@revs.ulaval.ca Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                          CO255135 638 bp mRNA linear EST 23-JUN-WS00824.B21_E09 WS-X-N-A-9 Picea glauca cDNA clone WS00824_E09
                                                                                                                                                                                                                                                      mRNA sequence.
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BST.
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Plate: 4b row: 01 column: B
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Fax: 418 656 7493
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Universite Laval
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: PolyTplus Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Entire strobilus"
/dev_stage="Three stages of preformed male strobili at end
of winter dormancy were pooled: swollen fully closed buds,
partly open buds and fully open buds"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ001: Male strobili developmental sequence"
/note="Norgan: Expanding male strobili; Vector: pBluescript
II SK (+) XR; Site_1: Eco-RI; Site_2: Xho-I; cDNA was
prepared from 5 mg of poly A+ selected RNA and was
directionally ligated into the pBluescript II SK (+) XR
vector (Stratagene), transformed by electroporation into
DH10B cells (In vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Picea glauca"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:3330"
'clone="GQ0014b_B01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="Tree 13-271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB
Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 608
     Kirkpatrick, R.,
., Babakaiff, R.,
                                                                                                                                                                                                                                                                                                       EST 23-JUN-2004
                                                                             Tracheophyta;
Picea.
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REFERENCE
AUTHORS
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ORGANISM
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CO209248/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 GTTCTACATAATGCGCCG 310
1 (bases 1 to 674)
Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R., Riu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R.,
                                                                                                                             Picea engelmannii x Picea sitchensis
Picea engelmannii x Picea sitchensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
                                                                                                                                                                                                                                                                                                                                                                                                        CO209248 674 bp mRNA linear EST 21-JUN-20 WS00914.B21 H17 IS-B-N-A-10 Picea engelmannii x Picea sitchensis cDNA clone \overline{W}S00914_H17 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               CO209248.1 GI:49021234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
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Plate: WS00824 row: E column: 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone
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/mol_type="mRNA"
/cultivar="pG-29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone="WS00824 E09"
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Canada, V6T 1Z3
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Picea engelmannii x Picea sitchensis

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VERSION
KEYWORDS
                                                                                                                                       RESULT 8
CO214192/c
LOCUS
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                                                                                                            DEFINITION
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                                                                                                                                                                                                                                                                                    323
                     WS00927.B21_D18 IS-B-N-A-10 Picea engelmannii CDNA clone WS00927_D18 3', mRNA sequence. CO214192. GI:49026638
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                                                                                                                                       CO214192
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Contact: Jeerg Bohlmann
Genome BC forest genomics program
University of British Columbia
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm.
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
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The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
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Plate: WS00914 row: H column: 17
                                                                                                                                                                                                                                                                              GTTCTACATAATGCGCCG 306
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Ask="Hermaphrodite"
/Ask="Hermaphrodite"
/Alab host="E. coli DH10B cells"
/Clone_lib="IS-B-N-A-10"
/note="Organ: Bark (with phloem and cambium attached) from
/note="Organ: Bark (with phloem and cambium attached) from
/note="Organ: Bark (with phloem and cambium attached) from
/note="Organ: Bark (with phloem and cambium one year old clonal trees grown under greenhouse
conditions in standard potting soil mixture; Vector:
phluescript II SK (+) XR; Sitte_1: EcoRI (5' end of cDNA);
Site_2: XhoI (3' end of cDNA); Bark was wounded using
razor blades along the entire length of the tree at 5 mm
intervals on opposite sides of the trunk. The same trees
solution resuspended in 0.1% (v/v) methyl jasmonate
solution resuspended in 0.1% (v/v) tween 20 (-59mLs per
tree). Bark tissue with phloem attached was harvested 3
hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8
days after initiating the treatment. Untreated control
bark was also harvested at time 0 hours. mRNA was isolated
from each tissue source independently and equal quantities
of mRNA from each tissue were then pooled. cDNA was
prepared from 5 micrograms of mRNA and directionally
ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR CDNA Library Construction Kit according
(Stratagene). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation. Normalization was applied according to
published methods [Bonaldo M.F. et al. (1996) Genome
highly expressed transcripts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 674
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/mol_type="mRNA"
/cultivar="Fal-1028"
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RESULT 9
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                                                                                                                                                                                                                               Local Similarity
                                                                                                               323
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The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
Unpublished (2004)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
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Tel: 1-604-822-0282
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Genome BC forest genomics program
University of British Columbia
  BI649133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bohlmann@interchange.ubc.ca
Plate: WS00927 row: D column: 18
High quality sequence stop: 674
                                                                                                                                       GTTCTACATAATGCGCCG 18
                                                                                                               GTTCTACATAATGCGCCG 306
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                         Interiorgan: Bark (with phloem and cambium attached) from one year old clonal trees grown under greenhouse conditions in standard potting soil mixture; Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Bark was wounded using razor blades along the entire length of the tree at 5 mm intervals on opposite sides of the trunk. The same trees were also sprayed with a 0.01% (v/v) methyl jasmonate solution resuspended in 0.1% (v/v) methyl jasmonate solution resuspended in 0.1% (v/v) tween 20 (-50mLs per tree). Bark tissue with phloem attached was harvested 3 hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8 days after initiating the treatment. Untreated control bark was also harvested at time 0 hours. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791) in order to reduce the abundance of highly expressed transcripts."
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/lab_host="E. coli DH10B cells"
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|mol_type="mRNA"
|cultivar="Fal-1028"
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'clone="WS00927_D18"
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                                                                                                                                                                                                     Score 18; DB
Pred. No. 25;
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DEFINITION
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                Unpublished (2003)
Other_ESTs: RTWW1_3_G12.b1_A015
Contact: Cordonnier-Pratt_MM
                                                                                                                                                                                                                                                                                                                                                                                                           RTWW1_3_G12.g1_A015 Well-watered loblolly pine roots taeda cDNA clone RTWW1_3_G12_A015 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603278931F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5319343 5',
Laboratory for Genomics and Bioinformatics
                                                                                                 An EST database from well-watered loblolly
                                                                                                                                                  Gebremedhin, M., Dervinia, C., Martin, T., White, T.,
                                                                                                                                                                          1 (bases 1 to 737)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W.,
                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                    Pinus taeda
                                                                                                                                                                                                                                                                                                         Pinus taeda (loblolly pine)
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National Institutes of Health, Mammalian Gene Collection
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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lone="IMAGE:5319343"
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                                                                                                    (Pinus
                                                                                                                                                    Davis, J. and
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                                                                                                                                                                                                                                Tracheophyta;
Pinus; Pinus.
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 807)
Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J., Wong, B., Warra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Ritland, K., and Bohlmann, J., Wong, G., Warra, M., Ellis, B.E., Douglas, C., Warra, W., Warra, 
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RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREY (CAGGAAACAGCTATGACC).
                                                                                                                                                                                                             Genome BC forest genomics program University of British Columbia UBC Biotechnology Laboratory, 6174 UVancouver, British Columbia, Canada, Tel: 1-604-822-0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WS00930.B21 A20 IS-B-N-A-10 Picea engelmannii x Picea sitchensis cDNA clone WS00930_A20 3', mRNA sequence.
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Picea engelmannii x Picea sitchensis
Bukaryota; Viridiplantae, Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                           Fax: 1-604-822-6097
Email: bohlmann@interchange.ubc.ca
Enail: Tow: A column: 20
Plate: W800930 row: A column: 20
High quality sequence stop: 807.
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Joerg Bohlmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
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/db_xref="taxon:3352"
/clone="RTWW1 3 G12 A015"
/lab_host="DH10B-T1 phage-resistant E. coli"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_llb="Well-watered loblolly pine roots WW1"
/clone_llb="Well-watered loblolly pine roots wite 2: Xho1; The
/note="Wector: pSL1180; Site 1: EcoRI; Site 2: Xho1; The
library was prepared from pOTyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL1180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."
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'strain="CCLONES"
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                 6174 University Boulevard,
Canada, V6T 1Z3
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Picea.
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BG517706
LOCUS
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SOURCE
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VERSION
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  FEATURES
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
Email: walbot@stanford.edu
Plate: 947070 row: C column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BG517706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG517706 303 bp mRNA linear EST 30-MAR-2001
947070C11.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
                                                                                                                                                                                                  Contact: Walbot V
                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                    Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG517706.1
                                                                          Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                  Stanford University
                                                                                                                                                                         Department of Biological Sciences
                                                                                                                                                                                                                                                   University
                                                                                                                                                                                                                                                                       Maize ESTs from various cDNA libraries sequenced
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                                                                                                                                                                                                                                                                                                                           (bases 1 to
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/clone | lib="15-B-N-A-10"
/clone | lib="15-B-N-A-10"
/note="Organ: Bark (with phloem and cambium attached) from
one year old clonal trees grown under greenhouse
conditions in standard potting soil mixture; Vector:
pBluescript II SK (+) XR; Site_1: EcoRI (5' end of cDNA);
Site 2: XhoI (3' end of cDNA); Bark was wounded using
razor blades along the entire length of the tree at 5 mm
intervals on opposite sides of the trunk. The same trees
were also sprayed with a 0.01% (v/v) methyl jasmonate
solution resuspended in 0.1% (v/v) tween 20 (-50mLs per
tree). Bark tissue with phloem attached was harvested 3
hours, 6 hours, 12 hours, 2 days, 4 days and 8
days after initiating the treatment. Untreated control
bark was also harvested at time 0 hours. mRNA was slolated
from each tissue source independently and equal quantities
of mRNA from each tissue were then pooled. cDNA was
prepared from each tissue were then pooled. cDNA was
prepared from each tissue were then booled. cDNA was
prepared from each tissue was then transformed by
electroporation into DNA was then transformed by
electroporation into DNA was then transformed by
published methods [Bonaldo M.F. et al. (1996) Genome
Research 6(9):791] in order to reduce the abundance of
highly expressed transcripts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Picea engelmannii x Picea sitchensis"
/mol type="mRNA"
/cultivar="Fal-1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli DH10B cells"
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Pred. No. 25;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of RNA prepared at the gorestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality
                                                                                                                                                                                                                                                                                                                                                                                                                                      16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAAAACGACGGCCAGT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 478)
1 (bases 1 to 478)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dea Gebremedhin, M., Dervinis, C., Martin, T., White, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF400102

478 bp mRNA linear EST 29-AUG-2003

RTWW1_3_G12.bl_A015 Well-watered loblolly pine roots WW1 Pinus

taeda cDNA clone RTWW1_3_G12_A015 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: RTWW1_3_G12.g1_A015
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                database from well-watered loblolly pine (Pinus taeda) roots
ished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf and stem, including leaf base"
/dev stage="2 week old seedling (3 leaves)"
/lab_host="XLI-Blue"
/clone_lib="947 - 2 week shoot from Barkan lab"
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
Site_1: EcoRI; Site_2: XhoI; Directionally cloned using
Stratagene's Unizap XR cDNA cloning kit with the 5' end
at the EcoRI site. The library represents 8 x 10e5
independent recombinant phage. The plants were greenhouse
/db_xref="taxon:3352"
/clone="RTWW1 3 G12 Al5"
/lab host="DHIOB-T1 phage-resistant E. coli"
/clone lib="Well-watered loblolly pine roots WW1"
/clone lib="Well-watered loblolly pine roots WW1"
/clone lib="Well-watered loblolly pine roots watered to EoRX; Site 2: XhoI; The library was prepared from poTyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
                                                                                                                                                                                                                                                    /organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
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/mol_type="mRNA"
/cultivar="B73"
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Pred. No. 2e-
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T., Davis,J. and
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VERSION KEYWORDS

ACCESSION DEFINITION

SOURCE

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COMMENT

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Matches

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17; Conserv
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Plate: 019 row: C column: 07
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Caixa Postal 6010, 13083-970, Campinas
Tel: 55 19 3788 1137
Pax: 55 19 3788 1089
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Clone distribution: clone distribution
through the Brazilian Clone Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centro de Biologia Molecular e Engenharia Genetica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA150538.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCBFRZ2019C07.g RZ2 Saccharum
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                                                          Similarity
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   GTTCTACATAATGCGCCG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: T7 Promoter Primer.
                                                                                                                    /note=Torgan: Shoot-root transition zone from young plants (small insert library); Vector: pSport1; Site_1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from [Shoot-root transition zone from young plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Saccharum officinarum"
                                                                                                                                                                                                                                                                                                                                                                                clone="SCBFRZ2019C07"
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94.4%;
                                                        91.1%;
                                                                                                                                                                                                                                                                                                                                                            host="DH10B"
                                                                                                                                                                                                                                                                                                                                           lib="RZ2"
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                                                        Score 16.4;
Pred. No. 2
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Pred. No. 2.1e+02;
0; Mismatches 1
                                        Mismatches
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                                                          .le+02;
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                                                                          <u>ه.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center (BCCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       information can be found
                                                                        Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 24-SEP-2003
                                     0;
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ACCESSION
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AUTHORS
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BE121144
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MEDLINE
PUBMED
                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 180-208,

(CARA) n#Simple repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE121144 524 bp mRNA linear EU-R-CAO-bau-e-11-0-UI.sl UI-R-CAO Rattus norvegicus UI-R-CAO-bau-e-11-0-UI 3', mRNA sequence.
BE121144 524 bp mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Pax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
Genome Res. 6 (9), 791-806 (1996)
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Forward POLYA=Yes.
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                             GTTCTACATAATGCGCCG 18
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol type="mRNA"
/strain="Sprague-Dawley"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="UI-R-CA0-bau-e-11-0-UI"
/lab host="DH10B (Life Technologies)"
/lab host="DH10B (Life Technologies)"
/lab host="UI-R-CA0"
/clone="UI-R-CA0"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CA0 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CA0 library is a subtracted library-derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Coarson Georgene Bosearyh 6.701-R06 1996)
                                                                                                                                                                                                                                                                                TAG_TISSUE=hippocampus
TAG_LIB=UI-R-CA0
                                                                                                                                                                                                                                                   TAG_SEQ=GATTG"
                                                                                                                                                                                                                                                                                                                                        Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                      91.1%; Score 16.4; DB 2; Length 524; 94.4%; Pred. No. 2.1e+02; tive 0; Mismatches 1; Indels
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Search completed: March 2, 2005, 03:05:19
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